

## **Composing the evolutionary puzzle of the remaining trout (*Salmo trutta* complex) diversity in Italy.**

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Mediterranean trout populations display a diversity of forms, representing a valuable model for the study of adaptation and a puzzling dilemma for taxonomists and biogeographers, rendered even more problematic by the widespread introgression of allochthonous (Atlantic) genes. Current Bayesian methods allow complex evolutionary models to be tested, offering the opportunity to statistically evaluate hypotheses about the evolutionary relationships of Mediterranean trout populations.

We used Approximate Bayesian Computation to test competing evolutionary scenarios for the main trout lineages ('marble' and Mediterranean 'brown' trout) autochthonous to the Italian basins, including the roles of geographical barriers and climate change in shaping the historical distribution of distinct lineages, and accounting for allochthonous introgression.

Our main results were that: i) the gene pool of the Adriatic endemic 'marble' trout started diverging earlier than the separation of Atlantic and Mediterranean lineages of 'brown' trout; ii) a relatively complex model of divergence, involving gene flow from Mediterranean 'brown' trout into the ancestral gene pool of marble trout is most consistent with the genetic data; iii) autochthonous gene pools of 'brown' trout in the Tyrrhenian and Adriatic basins of the Italian peninsula most likely diverged around the Last Glacial Maximum, indicating that movement along the coasts of southern Italy was possible as a result of climate/salinity conditions.

Our approach has, for the first time, allowed us to suggest an explicit model for the evolution of the main autochthonous trout lineages in Italy. We are currently using the same approach to test the hypothesis of speciation by hybridization in the Lake Garda endemic *Salmo carpio*.